

=> EIAV

L7 418 EIAV

=> S2 (1) mutation

35189 S2

249955 MUTATION

163778 MUTATIONS

311819 MUTATION

(MUTATION OR MUTATIONS)

L8 457 S2 (L) MUTATION

=> L7 and L8

L9 7 L7 AND L8

=> D L9 IBIB ABS 1-7

L9 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:467488 CAPLUS

DOCUMENT NUMBER: 145:6369

TITLE: The S2 accessory gene of equine infectious anemia virus is essential for expression of disease in ponies
AUTHOR(S): Fagerness, Angela J.; Flaherty, Maureen T.; Perry, Stephanie T.; Jia, Bin; Payne, Susan L.; Fuller, Frederick J.

CORPORATE SOURCE: Department of Public Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, NC, 27606-8401, USA

SOURCE: Virology (2006), 349(1), 22-30
CODEN: VIRLAX; ISSN: 0042-6822

PUBLISHER: Elsevier

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Equine infectious anemia virus (EIAV) is a macrophage-tropic lentivirus that persistently infects horses and causes a disease that is characterized by periodic episodes of fever, thrombocytopenia, and viremia. EIAV encodes only four regulatory/accessory genes, (tat, rev, ttm, and S2) and is the least genetically complex of all known lentiviruses. The authors sought to determine the role of the EIAV S2 accessory gene of EIAV by introducing mutations that would prevent S2 expression on the p19/wenv17 infectious mol. clone. Virus derived from the p19/wenv17 mol. clone is highly virulent and routinely fatal when given in high doses. In contrast, an S2 deletion mutant on the p19/wenv17 background is unable to induce acute disease and plasma virus loads were reduced by 2.5 to 4.0 logs at 15 days post-infection. The S2 deleted virus failed to produce any detectable clin. signs during a 5-mo observation period. These results demonstrate that S2 gene expression is essential for disease expression of EIAV.

REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:232971 CAPLUS

DOCUMENT NUMBER: 142:435581

TITLE: Discerning an effective balance between equine infectious anemia virus attenuation and vaccine efficacy

AUTHOR(S): Craigo, Jodi K.; Li, Feng; Steckbeck, Jonathan D.; Durkin, Shannon; Howe, Laryssa; Cook, Sheila J.; Issel, Charles; Montelaro, Ronald C.

CORPORATE SOURCE: Department of Molecular Genetics and Biochemistry, University of Pittsburgh, Pittsburgh, PA, USA

SOURCE: Journal of Virology (2005), 79(5), 2666-2677
CODEN: JOVIAM; ISSN: 0022-538X

PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Among the diverse exptl. vaccines evaluated in various animal lentivirus models, live attenuated vaccines have proven to be the most effective, thus providing an important model for examining critical immune correlates of protective vaccine immunity. We previously reported that an exptl. live attenuated vaccine for equine infectious anemia virus (EIAV), based on mutation of the viral S2 accessory gene, elicited protection from detectable infection by virulent virus challenge. To better understand the critical components of EIAV vaccine efficacy, we examine here the relationship between the extent of virus attenuation, the maturation of host immune responses, and vaccine efficacy in a comparative study of three related attenuated EIAV proviral vaccine strains: the previously described EIAVUKA S2 derived from a virulent proviral clone, EIAVUKA S2/DU containing a second gene mutation in the virulent proviral clone, and EIAVPRA S2 derived from a reference avirulent proviral clone. Inoculations of parallel groups of eight horses resulted in relatively low levels of viral replication (average of 102 to 103 RNA copies/mL) and a similar maturation of EIAV envelope-specific antibody responses as determined in quant. and qual. serol. assays. However, exptl. challenge of the exptl. immunized horses by our standard virulent EIAVPV strain by using a low-dose multiple exposure protocol (three inoculations with 10 median horse IDs, administered i.v.) revealed a marked difference in the protective efficacy of the various attenuated proviral vaccine strains that was evidently associated with the extent of vaccine virus attenuation, time of viral challenge, and the apparent maturation of virus-specific immunity.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2004:1102048 CAPLUS

DOCUMENT NUMBER: 142:174820

TITLE: Serological method using recombinant S2 protein to differentiate equine infectious anemia virus (EIAV)-infected and EIAV-vaccinated horses

AUTHOR(S): Jin, Sha; Issel, Charles J.; Montelaro, Ronald C.
CORPORATE SOURCE: Department of Molecular Genetics and Biochemistry, School of Medicine, University of Pittsburgh, Pittsburgh, PA, USA

SOURCE: Clinical and Diagnostic Laboratory Immunology (2004), 11(6), 1120-1129

CODEN: CDIMEN; ISSN: 1071-412X

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors recently reported a highly protective attenuated live virus vaccine for equine infectious anemia virus (EIAV) based on a proviral construct (EIAVUKA S2) with a genetically engineered mutation in the viral S2 gene that eliminates expression of this accessory protein. While the EIAVUKA S2 vaccine provides protection from detectable infection by exptl. challenge with highly virulent virus, the potential for com. application of this vaccine is complicated by the fact that horses inoculated with the EIAVUKA S2 vaccine strain become seropos. in various reference diagnostic assays based on detection of antibodies to virion core or envelope proteins. To address this issue, the authors describe here the development and optimization of a new serol. EIAV diagnostic ELISA to detect serum antibodies to the EIAV S2 protein that are produced in infected horses but not in horses inoculated with the EIAVUKA S2 vaccine virus. The test S2

protein antigen was developed using the S2 gene sequence from the EIAVUK strain of virus and a series of modifications to facilitate production and purification of the diagnostic antigen, designated HS2G. Using this

HS2G as antigen, the authors describe the development of an affinity ELISA that provides a sensitive and specific detection of S2-specific serum antibodies in exptl. and field-infected horses (22 of 24), without detectable reactivity with immune serum from uninfected or vaccinated horses. Thus, the S2-based diagnostic ELISA has the potential to accurately differentiate horses infected with EIAV from horses inoculated with an attenuated EIAV vaccine strain with a mutant S2 gene.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2004:934148 CAPLUS

DOCUMENT NUMBER: 141:409764

TITLE: Equine infectious anemia vaccine and diagnostic based on mutated S2 gene and/or DU gene

INVENTOR(S): Montelaro, Ronald C.; Craigo, Jodi; Li, Feng

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 31 pp., Cont.-in-part of U.S. Ser. No. 180,626.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004219166	A1	20041104	US 2003-627568	20030724
US 6585978	B1	20030701	US 2000-658547	20000909
US 2003165536	A1	20030904	US 2002-180626	20020626
US 7026113	B2	20060411		

PRIORITY APPLN. INFO.: US 2000-658547 A2 20000909
US 2002-180626 A2 20020626

AB The invention provides an equine infectious anemia (EIA) vaccine and/or construct that provides immunity to mammals, especially equines, from infection with equine infectious anemia virus (EIAV) and which, in embodiments, allows differentiation between vaccinated and non-vaccinated, but exposed, mammals or equines. In various embodiments, said vaccine encompasses at least one mutation in an EIAV which produces a non-functional gene in the vaccine virus that is always expressed in disease-producing wild-type EIA viruses. Addnl., said EIA vaccine virus cannot cause clin. disease in mammals or spread or shed to other mammals including equines. EIAV comprising mutated S2 gene (e.g. by introducing two redundant stop codons at amino acids G5 and G18) and/or DU gene, i.e. Δ S2, Δ DU or Δ S2 Δ DU, may be prepared as vaccine. The presence of S2 gene and/or DU gene, or antibodies to S2 protein and/or DU protein could be used for determination of whether an equine has been vaccinated with mutated EIAV or infected by wild-type EIAV.

L9 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2002:263898 CAPLUS

DOCUMENT NUMBER: 137:242771

TITLE: Proviral genomic sequence analysis of Chinese donkey leukocyte attenuated equine infectious anemia virus vaccine and its parental virus strain Liaoning

AUTHOR(S): Wang, Liu; Tong, Guangzhi; Liu, Hongquan; Yang, Zhibiao; Qiu, Huaji; Kong, Xiangang; Wang, Mei

CORPORATE SOURCE: National Key Laboratory of Veterinary Biotechnology,
Chinese Academy of Agricultural Sciences, Harbin,
150001, Peop. Rep. China
SOURCE: Science in China, Series C: Life Sciences (2002),
45(1), 57-67
CODEN: SCCLFO; ISSN: 1006-9305
PUBLISHER: Science in China Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Proviral DNA was extracted from donkey leukocyte infected with Chinese donkey leukocyte attenuated equine infectious anemia virus (DLA-EIAV), and peripheral blood lymphocytes (PBL) from a horse infected with the virulent EIAV strain Liaoning (EIAV L). The entire proviral DNA from both viruses was cloned and sequenced. The lengths of complete genomic sequences of DLA-EIAV and EIAV L provirus were 8266 bp and 8235 bp, resp. Sequence comparison indicated that DLA-EIAV shares 97.0% and 97.5% in sequence homol. with EIAV L and donkey-adapted EIAV (DA-EIAV), resp. Lots of variations occurred in long terminal repeat (LTR, consisting of U3, R, U5), ORF S2, and env regions between DLA-EIAV and EIAV L. The nucleotide sequence differences of the two viruses in U3, R, U5, ORF S2, and env are 13.2%, 7.5%, 5.1%, 3.9%, and 2.7%, resp., and predicted amino acid sequence differences in env and S2 coding regions are 4.4% and 8.8%, resp. Six conserved regions are characterized in Gp90. There is a cis-activating GATA motif in ENH of DLA-EIAV and EIAV L. Two N-linked glycosylation sites disappeared in DLA-EIAV Gp90 in comparison with that of EIAV L. A bHLH transcription factor binding consensus sequence was found in LTR of DLA-EIAV but not in EIAV L. Furthermore, there is a mutation in the stem of DLA-EIAV TAR resulting in formation of a uridine tuber. Further study is needed to uncover the relationship between sequence changes and their biol. functions of DLA-EIAV and L.

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2002:184924 CAPLUS
DOCUMENT NUMBER: 136:231232
TITLE: Equine infectious anemia vaccine
INVENTOR(S): Montalario, Ronald C.; Puffer, Bridget; Li, Feng;
Issel, Charles; Hennessey, Kristina J.; Brown, Karen K.
PATENT ASSIGNEE(S): Akzo Nobel N.V., Neth.
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002020041	A2	20020314	WO 2001-US27601	20010906
WO 2002020041	A3	20030109		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 6585978	B1	20030701	US 2000-658547	20000909

AU 2001088795 A5 20020322 AU 2001-88795 20010906
PRIORITY APPLN. INFO.: US 2000-658547 A 20000909
WO 2001-US27601 W 20010906

AB The invention provides an equine infectious anemia (EIA) vaccine that provides immunity to mammals, especially equines, from infection with equine infectious anemia virus (EIAV) and which allows differentiation between vaccinated and non-vaccinated, but exposed, mammals or equines. Preferably said vaccine encompasses at least one mutation in an EIAV which produces a non-functional gene in the vaccine virus that is always expressed in disease-producing wild-type EIA viruses. Addnl., said EIA vaccine virus cannot cause clin. disease in mammals or spread or shed to other mammals including equines.

L9 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2000:531206 CAPLUS

DOCUMENT NUMBER: 133:263688

TITLE: Mutations occurring during serial passage of Japanese equine infectious anemia virus in primary horse macrophages

AUTHOR(S): Zheng, Y.-H.; Sentsui, H.; Kono, Y.; Ikuta, K.

CORPORATE SOURCE: National Institute of Animal Health, Tsukuba, Ibaraki, Japan

SOURCE: Virus Research (2000), 68(1), 93-98

CODEN: VIREDF; ISSN: 0168-1702

PUBLISHER: Elsevier Science Ireland Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An attenuated equine infectious anemia virus (EIAV), named V26, was previously obtained after 50 passages of the Japanese virulent strain V70 in primary macrophage culture. To clarify the differences between both viruses, their full-length sequences were determined. There were higher mutations in S2 (6.15% amino acid difference) and LTR (10.7% nucleotide difference). The presumed initiation codon of the S2 gene was absent from the sequence of V26. There was a large insertion within the long-terminal repeat (LTR) U3 hypervariable region of V26. In addition, there were minor mutations in gag (1.22% amino acid difference), pol (1.05% amino acid difference) and env (1.65% amino acid difference) regions, but no mutation in tat region. No mutations were observed in the principal neutralizing domain in the gp90. Thus, the mutations in the S2 and LTR might be the major target sites of mutation in EIAV during serial passages in vitro.

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT